

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/836,544 C  
Source: IFW16  
Date Processed by STIC: 10/14/2005

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IFW16

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PATENT APPLICATION: US/09/836,544C

DATE: 10/14/2005  
TIME: 11:07:13

Input Set : A:\11-881.app  
Output Set: N:\CRF4\10142005\I836544C.raw

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3 <110> APPLICANT: Seed, Brian
4     Aruffo, Alejandro
5     Camerini, David
7 <120> TITLE OF INVENTION: CD27 Coding Sequence
9 <130> FILE REFERENCE: 11-88L
11 <140> CURRENT APPLICATION NUMBER: US 09/836,544C
12 <141> CURRENT FILING DATE: 2001-04-17
14 <150> PRIOR APPLICATION NUMBER: US 07/983,647
15 <151> PRIOR FILING DATE: 1992-12-01
17 <150> PRIOR APPLICATION NUMBER: US 07/553,759
18 <151> PRIOR FILING DATE: 1990-07-13
20 <150> PRIOR APPLICATION NUMBER: US 07/498,809
21 <151> PRIOR FILING DATE: 1990-03-23
23 <150> PRIOR APPLICATION NUMBER: US 07/379,076
24 <151> PRIOR FILING DATE: 1989-07-13
26 <150> PRIOR APPLICATION NUMBER: US 07/160,416
27 <151> PRIOR FILING DATE: 1988-02-25
29 <160> NUMBER OF SEQ ID NOS: 37
31 <170> SOFTWARE: PatentIn Ver. 2.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 2932
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
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39 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
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47 atactgtcct tctagtgttag ccgttagttag gccaaccatt caagaactct gtagcaccgc 180
49 ctacatacacct cgctctgtcta atccctgttac cagtggctgc tgccagtggc gataagtctg 240
51 gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg tcgggctgaa 300
53 cgggggggttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagatacc 360
55 tacagcgtga gctatgagaa agccgccacgc ttcccaagg gagaaggcg gacaggttac 420
57 cggtaagcgg cagggtcgg aacaggagac gcacgaggga gcttccaggg gaaacgcct 480
59 ggtatcttta tagtcctgtc gggtttcgccc acctctgact tgagcgtcga tttttgtat 540
61 gctcgtcagg gggcgaggc ctatggaaaa acgcccacaa cgccgaattt ccgcgggttt 600
63 tctcaacgtt acaacttaca gccgcgcgtc atttgcataatg atgcgccccg cttcccgata 660
65 agggagcagg ccagtaaaag cattaccgtt ggtgggttc ccgagcggcc aaaggagca 720
67 gactctaaat ctgcgtcat cgacttcgaa ggttcaatc cttcccccac caccatcaat 780
69 ttcaaaaatc cggaaatc tgcgtccgtc ttgtgtttt gagggtcgctg agtagtgcgc 840
71 gagtaaaatt taagctacaa caaggcaagg cttgaccgac aattgcataa agaatctgct 900
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75 attattgact agttataat agtaatcaat tacgggtca ttagttcata gcccataatat 1020  
77 ggagtccgc gttacataac ttacggtaaa tggccgcct ggctgaccgc ccaacgaccc 1080  
79 ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaataag ggactttcca 1140  
81 ttgacgtcaa tgggtggact attacggta aactgcccac ttggcagttac atcaagtgt 1200  
83 tcatatgcca agtacgcccc ctattgacgt caatgacggt aatggcccg cctggcatta 1260  
85 tgcccagttac atgacottat gggactttcc tacttggcag tacatctacg tattagtcat 1320  
87 cgctattacc atggtgatgc gttttggca gtacatcaat gggcggttat agcggttga 1380  
89 ctcacgggaa tttccaagtc tccacccat tgacgtcaat gggagttgt tttggcacca 1440  
91 aaatcaacgg gactttccaa aatgtcgtaa caactccgccc ccattgacgc aaatggccgg 1500  
93 aattcctggg cgggactggg gagtggcag ccctcagatg ctgcataataa gcagctgctt 1560  
95 tttgcctgta ctgggtctct ctgggttagac cagatctgag cctgggagct ctctggctaa 1620  
97 ctagagaacc cactgottaa gcctcaataa agcttctaga gatccctcga cctcgaggg 1680  
99 tcttcataac ctaccagtcc tgccctgca ggtcgccgccc gcgactctag aggatcttt 1740  
101 tgaaggaacc ttacttctgt ggtgtgacat aattggacaa actacctaca gagatttaaa 1800  
103 gctctaaggtaaataaaaa tttttaagtg tataatgtgt taaaactactg attctaattg 1860  
105 tttgtgtatt ttagattcca acctatggaa ctgatgaatg ggagcagttgg tggaaatgcct 1920  
107 ttaatgagga aaacctgttt tgctcagaag aaatgccatc tagtgtatgat gaggctactg 1980  
109 ctgactctca acattctact cctccaaaaa agaagagaaa ggtagaagac cccaggact 2040  
111 ttccctcaga attgotaagt ttggagtc atgctgtgtt tagtaataga actcttgctt 2100  
113 gctttgtat ttacaccaca aaggaaaaag ctgcaactgct atacaagaaa attatggaaa 2160  
115 aatattctgt aacctttata agtaggcata acaggtaaa tcataacata ctgtttttc 2220  
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121 gagatcataa tcagocatac cacatttgcgta gaggtttac ttgctttaaa aaacctccca 2400  
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125 gcagcttata atggttacaa ataaagcaat agcatcacaa atttcacaaa taaagcattt 2520  
127 ttttcaactgc attctagttg tggtttgcc aaactcatca atgtatctt tcatgtctgg 2580  
129 atccctgtgaa atgtgtgtca gttagggtgt ggaaagtccc caggctcccc agcaggcaga 2640  
131 agtatgcaaa gcatgcatct caattagtc gcaaccaggt gtggaaagtc cccaggctcc 2700  
133 ccagcaggca gaagtatgca aagcatgcat ctcaattagt cagcaaccat agtccccccc 2760  
135 ctaactccgc ccattccgcct ctaactccg cccagttccg cccattctcc gccccatggc 2820  
137 tgactaattt tttttattt tgcagaggcc gaggccgcct cggcctctga gctattccag 2880  
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143 <211> LENGTH: 1504  
144 <212> TYPE: DNA  
145 <213> ORGANISM: Homo sapiens  
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148 <221> NAME/KEY: CDS  
149 <222> LOCATION: (7)..(1059)  
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154 1 5 10  
156 ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc 96  
157 Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala  
158 15 20 25 30  
160 ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144  
161 Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro

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164	agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act			192
165	Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr			
166	50	55	60	
168	tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc			240
169	Ser Asp Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe			
170	65	70	75	
172	aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att			288
173	Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile			
174	80	85	90	
176	aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat			336
177	Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr			
178	95	100	105	110
180	gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att			384
181	Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile			
182	115	120	125	
184	caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca			432
185	Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr			
186	130	135	140	
188	acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg			480
189	Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu			
190	145	150	155	
192	tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac			528
193	Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His			
194	160	165	170	
196	aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac			576
197	Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn			
198	175	180	185	190
200	aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa			624
201	Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys			
202	195	200	205	
204	ggt ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc			672
205	Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu			
206	210	215	220	
208	ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa			720
209	Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys			
210	225	230	235	
212	aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac			768
213	Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His			
214	240	245	250	
216	aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct			816
217	Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala			
218	255	260	265	270
220	tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct			864
221	Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro			
222	275	280	285	
224	ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac			912
225	Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His			
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228 cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca 960  
229 Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr  
230 305 310 315  
232 caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag 1008  
233 Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln  
234 320 325 330  
236 cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct 1056  
237 Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser  
238 335 340 345 350  
240 aat taaaaaagat agaaaactgtc ttttcaata aaaagcactg tggatttctg 1109  
241 Asn  
243 ccctcctgat gtgcataatcc gtacttccat gaggtgttt ctgtgtgcag aacattgtca 1169  
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247 atctggagtt tttgggtctcc tcagagagct ccatacacacc agtaaggaga agcaatataa 1289  
249 gtgtgattgc aagaatggta gaggaccgag cacagaaatc ttagagattt cttgtcccct 1349  
251 ctcaggtcat gtgttagatgc gataaatcaa gtgattggtg tgcctgggtc tcactacaag 1409  
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268 20 25 30  
270 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe  
271 35 40 45  
273 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp  
274 50 55 60  
276 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu  
277 65 70 75 80  
279 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His  
280 85 90 95  
282 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr  
283 100 105 110  
285 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu  
286 115 120 125  
288 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu  
289 130 135 140  
291 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln  
292 145 150 155 160  
294 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp  
295 165 170 175  
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298 180 185 190  
300 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu  
301 195 200 205

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 306 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln  
 307 225 230 235 240  
 309 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val  
 310 245 250 255  
 312 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr  
 313 260 265 270  
 315 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His  
 316 275 280 285  
 318 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Gly His Arg Val  
 319 290 295 300  
 321 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val  
 322 305 310 315 320  
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 345 ctc agc gtg gtc tgc ctg cac tgc ttt ggt ttc atc agc tgt ttt 99  
 346 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe  
 347 15 20 25  
 349 tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147  
 350 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val  
 351 30 35 40 45  
 353 cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195  
 354 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp  
 355 50 55 60  
 357 aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt 243  
 358 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe  
 359 65 70 75  
 361 aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac 291  
 362 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr  
 363 80 85 90  
 365 aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat 339  
 366 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn  
 367 95 100 105  
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